

Fig. 1a

PGIA-01-A8	EVQLLESGGGLVQPGGSLRLSCAASGFTFS	SYAMS	WVRQAPGKGLEWVS	A	50
Vh3_DP-47__3-23_	EVQLLESGGGLVQPGGSLRLSCAASGFTFS	SYAMS	WVRQAPGKGLEWVS	A	
PGIA-01-A8	ISGSGGSTYYADSVKG	RFTISRDNKNTLYLQMNSLRAEDTAVYYCAK	DH	100	
Vh3_DP-47__3-23_	ISGSGGSTYYADSVKG	RFTISRDNKNTLYLQMNSLRAEDTAVYYCAK	.		
PGIA-01-A8	NYDSSGYLDY	WGQGTLLTVVSS	121	SEQ ID NO:140	
Vh3_DP-47__3-23_	.....	WGQGTLLTVVSS	JH1/JH4/JH5	SEQ ID NO:154	
PGIA-01-A8	NFMLTQPHSVSESPGKTVTISC	TRSSGSIAFDYVQ	WYQQRPGSAPTTVIY	50	
Vlambda6_6a	NFMLTQPHSVSESPGKTVTISC	TRSSGSIASNYVQ	WYQQRPGSSPTTVIY		
PGIA-01-A8	EDNQRP	GVPDRFSA	SIDSSNSASLTIS	ALKTEDEADYYC	100
Vlambda6_6a	EDNQRP	GVPDRFSG	SIDSSNSASLTIS	GLKTEDEADYYC	
PGIA-01-A8	V	FGGGTKLTVL	111	SEQ ID NO:141	
Vlambda6_6a	:	FGGGTKLTVL	JL2/JL3	SEQ ID NO:158	

Fig. 1b

PGIA-03-A9	QVQLQESGPGLVKPSGTL <del>SL</del> TC <del>AV</del> SGGSIS	<del>TS</del> DWWS	WVR <del>RP</del> PGKGLEWIG	50
Vh4_DP-70__4-04_	QVQLQESGPGLVKPSGTL <del>SL</del> TC <del>AV</del> SGGSIS	<del>SS</del> NWWS	WVR <del>Q</del> PPGKGLEWIG	
PGIA-03-A9	<del>E</del> IYHSGSTNYHP <del>SL</del> KS	RVTIS <del>L</del> DKSKNQFSLKLS <del>SV</del> TAADTA <del>VY</del> YCAR	<del>EG</del>	100
Vh4_DP-70__4-04_	<del>E</del> FYHSGSTNYNP <del>SL</del> KS	RVTIS <del>V</del> DKSKNQFSLKLS <del>SV</del> TAADTA <del>VY</del> YCAR	..	
PGIA-03-A9	<del>GH</del> SGSYPLIDY	WGKGT <del>L</del> VTVSS	121	SEQ ID NO:142
Vh4_DP-70__4-04_	.....	WG <del>Q</del> GTLVTVSS	JH4	SEQ ID NO:155
PGIA-03-A9	NFMLTQPHSVSESPGKTVTISC	<del>TR</del> SSGSIASNYVQ	WYQQRPGSSPTTVIY	50
Vlambda6_6a	NFMLTQPHSVSESPGKTVTISC	<del>TR</del> SSGSIASNYVQ	WYQQRPGSSPTTVIY	
PGIA-03-A9	<del>ED</del> NQRPS	GVPDRFSGSIDSSNSASLTISGLKTEDEADYYC	<del>Q</del> SYDSSNOG	100
Vlambda6_6a	<del>ED</del> NQRPS	GVPDRFSGSIDSSNSASLTISGLKTEDEADYYC	<del>Q</del> SYDSSN...	
PGIA-03-A9	<del>VV</del>	FGGGTKLTVL	112	SEQ ID NO:143
Vlambda6_6a	<del>..</del>	FGGGTKLTVL	JL2/JL3	SEQ ID NO:158

Fig 1c

PGIA-03-A11	QVQLVQSGP <u>EV</u> KKPGASV <u>EV</u> SKKASGYTFT	<u>GDYMH</u> WVRQAPGQ <u>PE</u> WMG	W	50
Vh1_DP-8_75__1-02__	QVQLVQSG <u>AE</u> EVKKPGASV <u>KV</u> SKKASGYTFT	<u>GYVMH</u> WVRQAPGQ <u>LE</u> WMG	W	
PGIA-03-A11	<u>INPQTGVTKYAQKFQ</u> RVTM <u>ARD</u> TSINTAYMEL <u>RGL</u> RSDDTAVYCV <u>R</u>	<u>ED</u>	I	100
Vh1_DP-8_75__1-02__	<u>INPNSGGTNYAQKFQ</u> RVTM <u>T</u> RDTSIS <u>T</u> AYMEL <u>SR</u> LRSDDDTAVYCA <u>R</u>			
PGIA-03-A11	<u>HNYDLMSAYNGLDV</u> WGQGTLLVTVSS 125			SEQ ID NO:144
Vh1_DP-8_75__1-02__	..... WGQGTLLVTVSS JH1			SEQ ID NO:156
PGIA-03-A11	QSVLTQPPSVSAAPGQKV <u>T</u> ISC	<u>SGSSSNIGNNHVS</u> WYQQL <u>A</u> GTAPKLL <u>I</u> F		50
Vlambda1_DPL5__1b__	QSVLTQPPSVSAAPGQKV <u>T</u> ISC	<u>SGSSSNIGNNYVS</u> WYQQL <u>P</u> GTAPKLL <u>I</u> Y		
PGIA-03-A11	<u>DNDKRPS</u> GIPDRFSGSKSGTSATLGITGLQTGDEADY <u>Y</u> C	<u>GTWDKSPTDIY</u>		100
Vlambda1_DPL5__1b__	<u>DNNKRPS</u> GIPDRFSGSKSGTSATLGITGLQTGDEADY <u>Y</u> C	<u>GTWDSLSA</u>		
PGIA-03-A11	<u>V</u> FG <u>S</u> GTKLTVL 111			SEQ ID NO:145
Vlambda1_DPL5__1b__	<u>V</u> FG <u>T</u> GTKVTVL JL1			SEQ ID NO:159

Fig. 1d

PGIA-03-B2	QVQLQESGPGGLVKPSA	TL	SLTCAVSGGSIS	SNHWNS	WVRQSPGKGLEWIG	50
Vh4_DP-70__4-04_	QVQLQESGPGGLVKPSG	TL	SLTCAVSGGSIS	SSNWNNS	WVRQPPGKGLEWIG	
PGIA-03-B2	EIYTYGGAGANYNP	SLKS	RVDISMDKSKNQFSL	HLSSVTAADTAVYCGR	HL	100
Vh4_DP-70__4-04_	EIYHSGSTNYNP	SLKS	RVTISVDKSKNQFSL	KLSSVTAADTAVYCAR	..	
PGIA-03-B2	TGYDCFDI	WGQGT	LVTVSS	119	SEQ ID NO:148	
Vh4_DP-70__4-04_	.....	WGQGT	LVTVSS	JH4	SEQ ID NO:155	
PGIA-03-B2	QAVLTQPPSSVSGAPGQ	RV	TISC	TGSSSNIGAGYDVH	WYQQLPGTAPKLLI	50
Vlambda1_DPL8__1e_	QSVLTQPPSVSGAPGQ	RV	TISC	TGSSSNIGAGYDVH	WYQQLPGTAPKLLI	
PGIA-03-B2	Y GNSNRPS	GVPDR	FGSKSGTSASLAITGLQAEDEADYIC	QSYDSSLSGV	100	
Vlambda1_DPL8__1e_	Y GNSNRPS	GVPDR	FGSKSGTSASLAITGLQAEDEADYIC	QSYDSSLSG.		
PGIA-03-B2	FGTGTQLTVL	110			SEQ ID NO:149	
Vlambda1_DPL8__1e_	FGGGTQLTVL	JL7			SEQ ID NO:160	

Fig 1e

PGIA-04-A5	QVQLQESGPGLVKPSGTL <del>SL</del> LTCAVSGGSIS	<del>TSDWWS</del>	WVR <del>R</del> PPGKGLEWIG	50
Vh4_DP-70__4-04_	QVQLQESGPGLVKPSGTL <del>SL</del> LTCAVSGGSIS	<del>SSNWWS</del>	WVR <del>Q</del> PPGKGLEWIG	
PGIA-04-A5	<del>EIYHSGSTNYHP</del> SLKS	RVTIS <del>LD</del> DKSKNQFSLKLSVTAADTA	VYYCAR	<del>EG</del> 100
Vh4_DP-70__4-04_	<del>EIYHSGSTNYNP</del> SLKS	RVTIS <del>VD</del> DKSKNQFSLKLSVTAADTA	VYYCAR	..
PGIA-04-A5	<del>GHSGSYPLDY</del>	WGRGTLVTVSS	121	SEQ ID NO:150
Vh4_DP-70__4-04_	.....	WGRGTLVTVSS	JH2	SEQ ID NO:155
PGIA-04-A5	NFMLTQPHSVSESPGK <del>TAT</del> IS	<del>TGSGGSIARS</del> YVQ	WYQQRPGR <del>APSI</del> VIY	50
Vlambda6_6a	NFMLTQPHSVSESPGK <del>TVT</del> IS	<del>TRSSGSIASN</del> YVQ	WYQQRP <del>GSSP</del> TTVIY	
PGIA-04-A5	<del>EDYQ</del> RPS	GVPDRFSGSIDSSSNSASLTITGLKT <del>D</del> EADYYC	<del>QSSDDNNNV</del>	100
Vlambda6_6a	<del>EDNQR</del> RPS	GVPDRFSGSIDSSSNSASLTISGLKT <del>E</del> EADYYC	<del>QSYDSSN</del> ..	
PGIA-04-A5	<del>V</del>	FGGGTKVTVL	111	SEQ ID NO:151
Vlambda6_6a	<del>V</del>	FGGGTKVTVL	JL2/JL3	SEQ ID NO:158

Fig 1f

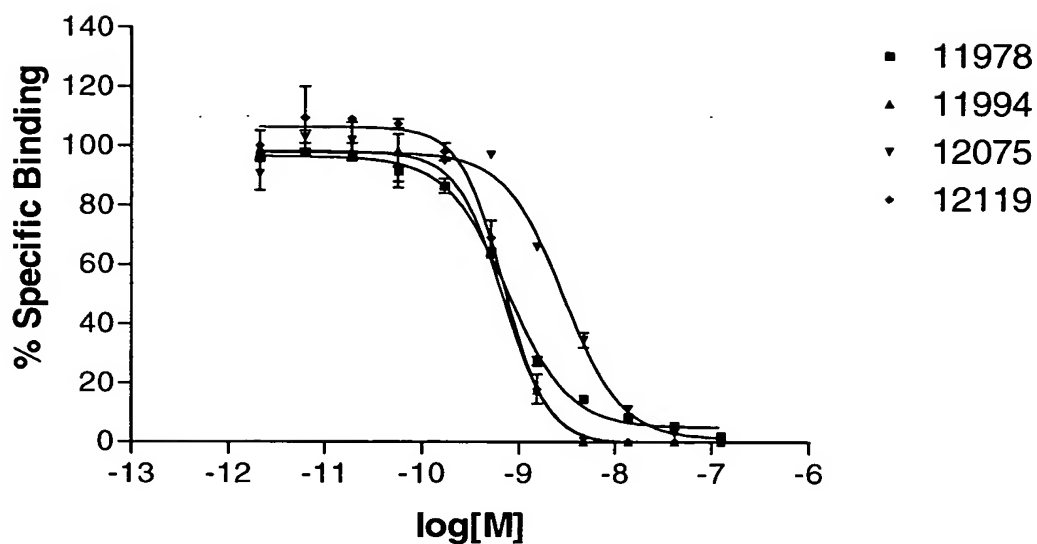
PGIA-04-A8	QVQLQESGPGLVKPSSETLSLTCTNVSGGSIR	NYFWS	WIRQPPGQGLEWIG	Y	50
Vh4_DP-71__4-59_	QVQLQESGPGLVKPSSETLSLTCTVSGGSIS	SYFWS	WIRQPPGKGLEWIG	Y	
PGIA-04-A8	IYVSGTTDYNPSLKG	RVTISL	DTSKTQFSLKLSVTAADTA	FYYCVR	GPN 100
Vh4_DP-71__4-59_	IYVSGSTNYPNPSLKS	RVTISV	DTSKNQFSLKLSVTAADTA	VYYCAR	...
PGIA-04-A8	KYAFDP	WGQGLVTVSS	117		SEQ ID NO:152
Vh4_DP-71__4-59_	.....	WGQGLVTVSS	JH4		SEQ ID NO:157
PGIA-04-A8	SYELTQPPSVSVSPGQTASITC	SGDKLGDKFAS	WYQQK	AGQSPVLVIY	RD 50
Vlambda3_DPL23__3r_	SYELTQPPSVSVSPGQTASITC	SGDKLGDKYAC	WYQQK	PGQSPVLVIY	QD
PGIA-04-A8	TKRPS	GIPERFSGNSGNTATLTISGTQAMDEADYYC	QAWDSSTAV	FGTG	100
Vlambda3_DPL23__3r_	SKRPS	GIPERFSGNSGNTATLTISGTQAMDEADYYC	QAWDSSTA	FGTG	
PGIA-04-A8	TKVTVL	106			SEQ ID NO:153
Vlambda3_DPL23__3r_	TKVTVL	JL1			SEQ ID NO:161

Fig. 19

PGIA-05-A1	QQLQESGPGLVKPSGTLTLTCAVSGGSIS	TSDWWS	WVRPPPGKGLEWIG	50
Vh4_DP-70__4-04_	QVQLQESGPGLVKPSGTLTLTCAVSGGSIS	SSNWWS	WVRQPPGKGLEWIG	
PGIA-05-A1	ETVHSGSTNYHPSLKS	RVTISL	DKSKNQFSLKLSVTAADTAVYCAR	EG 100
Vh4_DP-70__4-04_	ETVHSGSTNYNPSLKS	RVTISV	DKSKNQFSLKLSVTAADTAVYCAR	..
PGIA-05-A1	GHSGSYPLIDY	WGRGTLVTVSS	121	SEQ ID NO:146
Vh4_DP-70__4-04_	.....	WGRGTLVTVSS	JH2	SEQ ID NO:155
PGIA-05-A1	NFMLTQPHSVSESPGKTVTISC	ARSSGSIASNYVQ	WYQQRPGSSPTTIIY	50
Vlambda6_6a	NFMLTQPHSVSESPGKTVTISC	TRSSGSIASNYVQ	WYQQRPGSSPTTVIY	
PGIA-05-A1	EDRQRPS	GVPDRFSGSIDSSSNSASLTISGLKTEDEADYYC	QSYDSSDHV	100
Vlambda6_6a	EDNQRP	GVPDRFSGSIDSSSNSASLTISGLKTEDEADYYC	QSYDSSN	
PGIA-05-A1	V	FGGGTKLTVL	111	SEQ ID NO:147
Vlambda6_6a	;	FGGGTKLTVL	JL2/JL3	SEQ ID NO:158

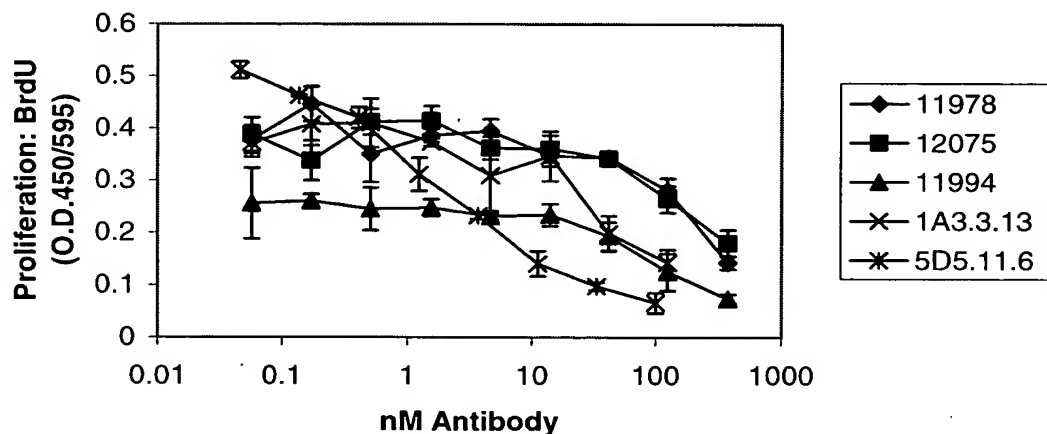
## Figure 2

### c-Met IgG Antibodies In Europium Ligand Competition Assay



## Figure 3

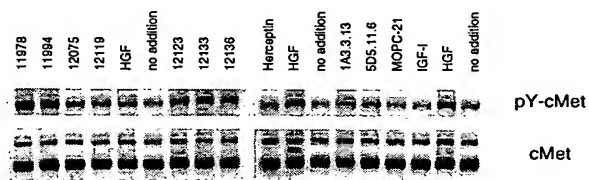
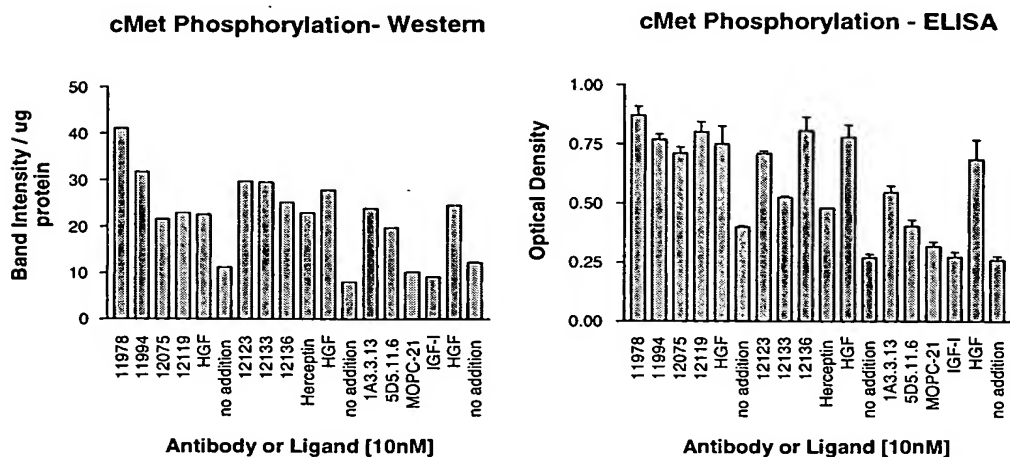
### Inhibition of 184B5 Proliferation (0.133 nM rhHGF) by IgG





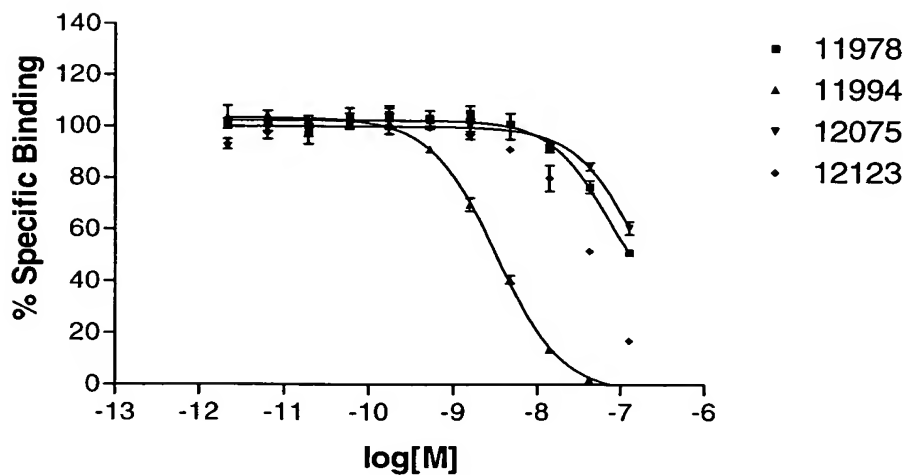
# Figure 4

## Tyrosine Phosphorylation of c-Met by c-Met IgG Antibodies



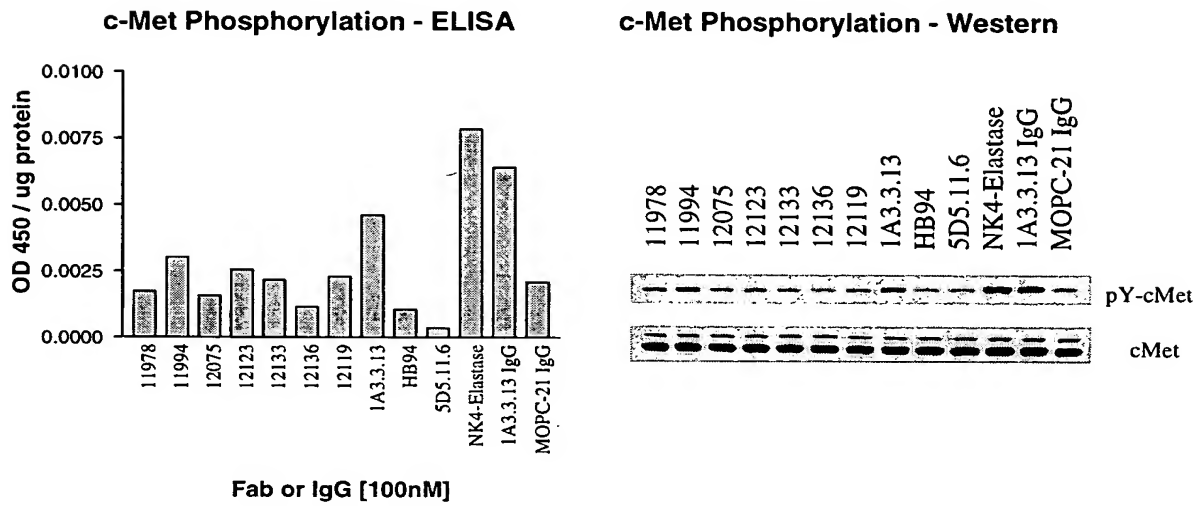
# Figure 5

## c-Met Fab in Europium Ligand Competition Assay

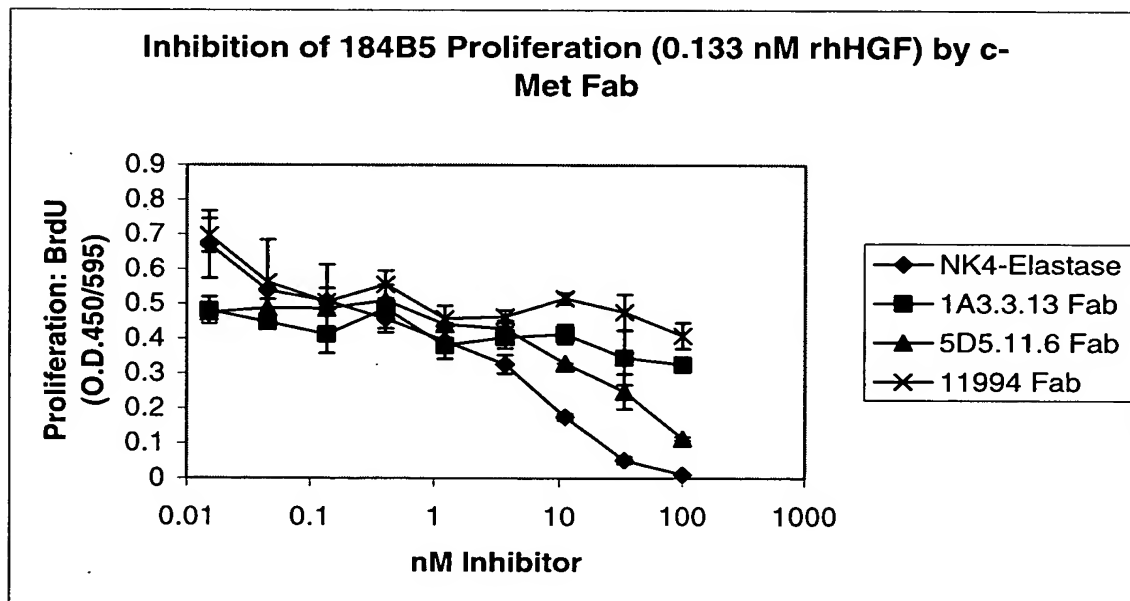


# Figure 6

## Tyrosine Phosphorylation of c-Met by c-Met Fab

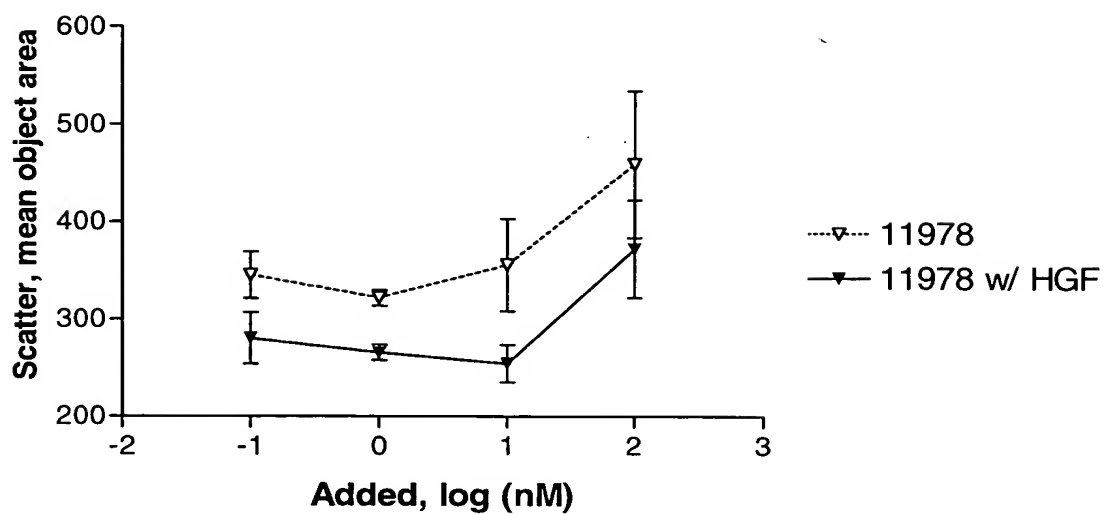


# Figure 7



# Figure 8

## DU145 Scatter Assay With A c-Met IgG Antibody



# Fig. 9

## Inhibition of HGF Induced Migration by anti c-met Antibodies in the Presence of 225pM HGF

